Attachment.

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form: .

Application Serial Number: ___10/564,136___

Source: ___IFWO___

Date Processed by STIC: ___10/31/2006___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: _10/564,136_ |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
   Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
   prevent "wrapping."

2____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
   Numbering   use space characters, instead.

4____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. **Please**
   ensure your subsequent submission is saved in ASCII text.

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,**
   each n or Xaa can only represent a single residue. Please present the maximum number of each
   residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
   "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
   previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
   the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for**
   Artificial or Unknown sequences.

7____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
   (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   This sequence is intentionally skipped
   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
   27 thru 215

8____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
   (NEW RULES)   <210> sequence id number
   <400> sequence id number
   000

9____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
   (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
   Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
   is Artificial Sequence. (see item 11 below)

11____Use of <220>   Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use
   of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
   Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
   explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
   Sequence Rules

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
   "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
   listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa   "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

IFWO

RAW SEQUENCE LISTING　　　　　　　　DATE: 10/31/2006
PATENT APPLICATION:　US/10/564,136　　TIME: 15:10:35

Input Set : A:\10564136.RAW
Output Set: N:\CRF4\10312006\J564136.raw

```
  3 <110> APPLICANT: Olson-Munoz, Marilyn C.
  4         Curtis, Michelle L.
  5         Ip, Hon S.
  6         Kwiatkowski, Robert W., Jr.
  7        'Armantrout, Kyle C.
  8         Cao, Peng
  9         Hurwitz, Bonnie L.
 10         Machmeier, Daniel K.
 11         Olson, Sarah M.
 12         Chehak, LuAnne
 14 <120> TITLE OF INVENTION: Assays for the Direct Measurement of Gene Dosage
 16 <130> FILE REFERENCE: FORS-10718
 18 <140> CURRENT APPLICATION NUMBER: US/10/564,136
 18 <141> CURRENT FILING DATE: 2006-01-10
 18 <160> NUMBER OF SEQ ID NOS: 230
 20 <170> SOFTWARE: PatentIn version 3.3
```

C--> 18
C--> 18
E--> 18

Does Not Comply Corrected Diskette Needed (pg-1)

→ *found 39*

ERRORED SEQUENCES

```
243 <210> SEQ ID NO: 26
244 <211> LENGTH: 25
245 <212> TYPE: DNA
246 <213> ORGANISM: Homo sapiens
248 <400> SEQUENCE: 26
249 cgcgccgagg cctgagcaac gtgca
362 <210> SEQ ID NO:
362 <211> LENGTH:
362 <212> TYPE:
362 <213> ORGANISM:
362 <400> SEQUENCE: 215
363 gagattgtgc acgaggactt gaagatgggg tctgatgggg agagtgacca ggcttcagcc    60
365 acgtcctcgg atgaggtgca gtctccagtg a                                   91
368 <210> SEQ ID NO: 216
```

E--> 249
E--> 362
E--> 362
E--> 362
E--> 362
E--> 362
E--> 368

25 ②

—27

*Missing Sequence from 27 thru 215.—
for Intentionally Skipped Sequences.
Pls us this format . 210 000 } See Item 8
400 000 } on Error
Summary
Sheet.*

10/31/2006

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/31/2006
PATENT APPLICATION: US/10/564,136   TIME: 15:10:36

Input Set : A:\10564136.RAW
Output Set: N:\CRF4\10312006\J564136.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:26; Line(s) 249,250,251,252,253,254,255,256,257,258,259,260,261,262
Seq#:26; Line(s) 263,264,265,266,267,268,269,270,271,272,273,274,275,276
Seq#:26; Line(s) 277,278,279,280,281,282,283,284,285,286,287,288,289,290
Seq#:26; Line(s) 291,292,293,294,295,296,297,298,299,300,301,302,303,304
Seq#:26; Line(s) 305,306,307,308,309,310,311,312,313,314,315,316,317,318
Seq#:26; Line(s) 319,320,321,322,323,324,325,326,327,328,329,330,331,332
Seq#:26; Line(s) 333,334,335,336,337,338,339,340,341,342,343,344,345,346
Seq#:26; Line(s) 347,348,349,350,351,352,353,354,355,356,357,358,359,360
Seq#:26; Line(s) 361

Skipped Sequences(NEW RULES):
Sequence(s)__missing. If intentional, please use the following format for
each skipped sequence.
<210> sequence id number
<400> sequence id number
.000

Seq#:27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50
Seq#:51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74
Seq#:75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98
Seq#:99,100,101,102,103,104,105,106,107,108,109,110,111,112,113,114,115,116
Seq#:117,118,119,120,121,122,123,124,125,126,127,128,129,130,131,132,133,134
Seq#:135,136,137,138,139,140,141,142,143,144,145,146,147,148,149,150,151,152
Seq#:153,154,155,156,157,158,159,160,161,162,163,164,165,166,167,168,169,170
Seq#:171,172,173,174,175,176,177,178,179,180,181,182,183,184,185,186,187,188
Seq#:189,190,191,192,193,194,195,196,197,198,199,200,201,202,203,204,205,206
Seq#:207,208,209,210,211,212,213,214,215

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/564,136

DATE: 10/31/2006
TIME: 15:10:36

Input Set : A:\10564136.RAW
Output Set: N:\CRF4\10312006\J564136.raw

L:18 M:270 C: Current Application Number differs, Replaced Current Application No
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:187 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:
L:249 M:254 E: No. of Bases conflict, LENGTH:Input:2 Counted:25 SEQ:26
L:362 M:282 E: Numeric Field Identifier Missing, <210> is required.
L:362 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:362 M:282 E: Numeric Field Identifier Missing, <212> is required.
L:362 M:282 E: Numeric Field Identifier Missing, <213> is required.
L:362 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:26 differs:215
L:368 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 27 thru 215
L:18 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (230) Counted (39)